Amendments to the Claims:

Please cancel claims 1-54 and add new claims 55-81. This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

55. (New): A method comprising the steps of:

a) obtaining a biological sample;

b) generating a gene expression profile of the sample, thereby identifying a mRNA expressed in the sample;

c) determining the nucleotide sequence of the mRNA;

d) predicting the amino acid sequence of the polypeptide encoded by the mRNA;

e) predicting the mass of the encoded polypeptide;

f) generating a protein profile of polypeptides in the sample by mass spectrometry; and

g) determining the presence or absence in the protein profile of a polypeptide having a mass that correlates to the predicted mass of the encoded polypeptide.

56. (New): The method of claim 55, wherein the biological sample comprises a cell lysate from a healthy cell.

57. (New): The method of claim 55, wherein the biological sample comprises a cell lysate from a pathological cell.

58. (New): The method of claim 55, wherein the biological sample comprises a cell lysate from a cell contacted by a toxic compound.

59. (New): The method of claim 55, wherein the biological sample comprises a cell lysate from a cell of a subject who responds to a drug treatment.

60. (New): The method of claim 55, wherein the biological sample comprises a cell lysate from a cell of a subject who does not respond to a drug treatment.

61. (New): The method of claim 55, wherein the biological sample comprises a human cell.

62. (New): The method of claim 55, wherein the step of generating the gene expression profile comprises identifying expressed mRNA with a nucleic acid array.

63. (New): The method of claim 55, wherein the step of generating the gene expression profile comprises identifying expressed mRNA with an oligonucleotide array.

64. (New): The method of claim 55, wherein the step of generating the gene expression profile comprises identifying expressed mRNA with an mRNA array.

65. (New): The method of claim 55, wherein the step of generating the gene expression profile comprises identifying expressed mRNA with an EST array.

66. (New): The method of claim 55, wherein the step of generating the gene expression profile comprises identifying expressed mRNA with a northern blot or a dot blot.

67. (New): The method of claim 55, wherein the mRNA is differentially expressed in two biological samples.

68. (New): The method of claim 67, wherein the two biological samples are derived from a normal cell and a pathologic cell.

69. (New): The method of claim 68, wherein the pathologic cell is a cancer cell.

70. (New): The method of claim 67, wherein the two biological samples are derived from a healthy cell and a cell exposed to a toxic compound.

71. (New): The method of claim 55, wherein mass spectrometry is laser desorption/ionization mass spectrometry.

72. (New): The method of claim 55, wherein mass spectrometry is electrospray mass spectrometry.

73. (New): The method of claim 55, further comprising,

in step (d), predicting a post-translational modification of the encoded polypeptide;

in step e), predicting the mass of the encoded polypeptide to reflect the post-translational modification; and

in step g), determining the presence or absence of a polypeptide having a mass that correlates to the predicted mass of the encoded polypeptide having the post-translational modification.

74. (New): The method of claim 73, wherein the post-translational modification is phosphorylation or glycosylation.

75. (New): The method of claim 55 further comprising:

(i) predicting at least one physio-chemical characteristic of the encoded polypeptide selected from the group consisting of isoelectric point, hydrophobicity, hydrophilicity, glycosylation, phosphorylation, epitope sequence, ligand binding sequence, and metal chelate binding;

(ii) fractionating the polypeptides in the sample according to the at least one physiochemical characteristic before step (f); and

(iii) in step (g), correlating the predicted mass and the at least one physiochemical characteristic of the encoded polypeptide with a polypeptide in the protein expression profile.

76. (New): The method of claim 75, wherein the physio-chemical characteristic is isoelectric point and fractionating the polypeptides comprises isoelectric focusing.

77. (New): The method of claim 75, wherein the physiochemical characteristic is isoelectric point and fractionating the polypeptides comprises capturing polypeptides on a solid phase-

bound ion exchange adsorbent, washing away unbound polypeptides and detecting the bound polypeptides by laser desoprtion/ionization mass spectrometry.

78. (New): The method of claim 75, wherein the physiochemical characteristic is hydrophobicity and fractionating the polypeptides comprises capturing polypeptides on a solid phase-bound hydrophobic interaction adsorbent, washing away unbound polypeptides and detecting the bound polypeptides by laser desoprtion/ionization mass spectrometry.

79. (New): The method of claim 75, wherein the physiochemical characteristic is hydrophilicity and fractionating the polypeptides comprises capturing polypeptides on a solid phase-bound hydrophilic interaction adsorbent, washing away unbound polypeptides and detecting the bound polypeptides by laser desoprtion/ionization mass spectrometry.

80. (New): The method of claim 75, wherein the physiochemical characteristic is epitope sequence and fractionating the polypeptides comprises capturing polypeptides on a solid phase-bound biospecific adsorbent, washing away unbound polypeptides and detecting the bound polypeptides by laser desoprtion/ionization mass spectrometry.

81. (New): The method of claim 75, wherein the physiochemical characteristic is metal chelate binding and fractionating the polypeptides comprises capturing polypeptides on a solid phase-bound immobilized metal chelate adsorbent, washing away unbound polypeptides and detecting the bound polypeptides by laser desoprtion/ionization mass spectrometry.